Applicant: Brian McKeown U.S. Serial No.: 10/632,393 U.S. Filing Date: August 1, 2003 Response to Final Office Action

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Please amend the above-identified application as follows:

## Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-50 (canceled)

51. (currently amended): A method of performing a primer extension reaction to identify variant nucleotides of target nucleic acids using chain terminators, comprising:

obtaining an amplicon having a sequence generated from a target nucleic acid and a sequence generated from a first strand amplification primer, by amplifying a target nucleic acid having a nucleotide sequence containing a variant nucleotide flanked by an invariant nucleotide, wherein the first strand amplification primer employed to generate the sequence from the first strand amplification primer comprises a 5' tag substantially incapable of hybridizing to the target nucleic acid under amplification conditions, and wherein the 5' tag contains the same nucleotide bases in sequence as at least the variant nucleotide and the invariant nucleotide of the target nucleic acid, and employing a second strand amplification primer;

employing the amplicon in a primer extension reaction wherein the identity of the variant nucleotide in the sequence generated from the target nucleic acid is determined by hybridizing a first identification primer immediately adjacent to the variant nucleotide in the sequence generated from the target nucleic acid;

hybridizing a second identification primer immediately adjacent to the variant nucleotide in the sequence generated from the 5' tag of the first strand amplification primer;

extending the first and the second identification primers in the presence of [[one]] two or more chain terminators and a polymerizing agent; and

determining the identity of the variant nucleotide generated from the target nucleic acid; and by\_comparing extension product of the first identification primer and extension product of the second identification primer to identify the variant nucleotide of the target nucleic acid, thereby performing the primer extension reaction.

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52. (currently amended): A method according to claim 51, wherein the variant nucleotide of the target ean be is a wild-type nucleotide base or mutant nucleotide base, and at least two first strand amplification primers are employed, each first strand amplification primer having a 5' nucleic acid tag, the first 5' tag of the at least two first strand amplification primers comprises the same nucleotide base as the mutant nucleotide base and the second 5' tag of the at least two first strand amplification primers comprises the same nucleotide base as the wild-type nucleotide base, the first 5' tag and the second 5' tag being employed at a known ratio in the primer extension reaction so that a population of amplicons is generated having the wild-type and mutant nucleotide base represented at [[a]] the known ratio from the first and second 5' tags.

## 53-61 (cancelled)

- 62. (previously presented): A method according to claim 52, wherein the first 5' tag and the second 5' tag differ from each other by one nucleotide base.
- 63. (previously presented): A method according to claim 62, wherein the one nucleotide base that the first and the second 5' tag differ is the same nucleotide base as the wild-type or the mutant nucleotide base.
- 64. (previously presented): A method according to claim 51, wherein the target nucleic acid comprises nucleic acids from two or more individuals.
- 65. (previously presented): A method according to claim 64, wherein at least one of the two or more individuals displays at least one complex genotype.
- 66. (previously presented): A method according to claim 51, wherein the chain terminator is a dideoxynucleotide or an acyclo terminator.

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- 67. (currently amended): A method according to claim 51, wherein the chain terminator is terminators are labeled.
- 68. (previously presented): A method according to claim 51, wherein the identification primers comprise a tag capture moiety.
- 69. (new): A method according to claim 51, wherein the target nucleic acid comprises the scrapie locus.